

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: MAERTENS, GEERT
BOSMAN, FONS
DE MARTYNOFF, GUY
BUYSE, MARIE-ANGE

(ii) TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

(iii) NUMBER OF SEQUENCES: 111

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NIXON & VANDERHYE P.C.
(B) STREET: 1100 NORTH GLEBE ROAD
(C) CITY: ARLINGTON
(D) STATE: VIRGINIA
(E) COUNTRY: U.S.A.
(F) ZIP: 22201-4714

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/612,973
(B) FILING DATE: 11-MAR-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BYRNE, THOMAS E.
(B) REGISTRATION NUMBER: 32,205
(C) REFERENCE/DOCKET NUMBER: 1487-10

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703) 816-4000
(B) TELEFAX: (703) 816-4100

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCATGCAAG CTTAATTAAT T

21

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT

60

TAACTGCA

68

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..639

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys
1 5 10 15

48

CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met
20 25 30

96

TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA

144

| | | | |
|---|-----|-----|-----|
| Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala | | | |
| 35 | 40 | 45 | |
| GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG | | | 192 |
| Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu | | | |
| 50 | 55 | 60 | |
| AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT | | | 240 |
| Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala | | | |
| 65 | 70 | 75 | 80 |
| AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG | | | 288 |
| Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu | | | |
| 85 | 90 | 95 | |
| CTC GTT GGG GCG GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC | | | 336 |
| Leu Val Gly Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu | | | |
| 100 | 105 | 110 | |
| TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC | | | 384 |
| Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg | | | |
| 115 | 120 | 125 | |
| CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC | | | 432 |
| Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His | | | |
| 130 | 135 | 140 | |
| ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT | | | 480 |
| Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro | | | |
| 145 | 150 | 155 | 160 |
| ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC | | | 528 |
| Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val | | | |
| 165 | 170 | 175 | |
| GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC | | | 576 |
| Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala | | | |
| 180 | 185 | 190 | |
| TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA | | | 624 |
| Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu | | | |
| 195 | 200 | 205 | |
| CTC TTT GCT CTC TAATAG | | | 642 |
| Leu Phe Ala Leu | | | |
| 210 | | | |

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

| | | | |
|---|---|----|----|
| Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys | | | |
| 1 | 5 | 10 | 15 |

Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met
20 25 30

Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala
35 40 45

Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu
50 55 60

Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala
65 70 75 80

Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu
85 90 95

Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu
100 105 110

Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg
115 120 125

Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His
130 135 140

Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro
145 150 155 160

Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val
165 170 175

Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala
180 185 190

Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu
195 200 205

Leu Phe Ala Leu
210

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 795 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..792

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

| | |
|--|-----|
| ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu | 48 |
| 1 5 10 15 | |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg | 96 |
| 20 25 30 | |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala | 144 |
| 35 40 45 | |
| ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu | 192 |
| 50 55 60 | |
| CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val | 240 |
| 65 70 75 80 | |
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val | 288 |
| 85 90 95 | |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys | 336 |
| 100 105 110 | |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr | 384 |
| 115 120 125 | |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His | 432 |
| 130 135 140 | |
| GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val | 480 |
| 145 150 155 160 | |
| GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile | 528 |
| 165 170 175 | |
| TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr | 576 |
| 180 185 190 | |
| CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn | 624 |
| 195 200 205 | |
| TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro | 672 |
| 210 215 220 | |

| | |
|---|-----|
| CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG | 720 |
| Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala | |
| 225 230 235 240 | |
| GGT CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT | 768 |
| Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile | |
| 245 250 255 | |
| GTG ATG CTA CTC TTT GCT CCC TAATAG | 795 |
| Val Met Leu Leu Phe Ala Pro | |
| 260 | |

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
 1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
 50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
 85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
 100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
 130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
 145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
 165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
 180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
 195 200 205
 Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 210 215 220
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala
 225 230 235 240
 Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile
 245 250 255
 Val Met Leu Leu Phe Ala Pro
 260

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..630

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

| | |
|---|-----|
| ATG TTG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGC TTC GCC GAC CTC | 48 |
| Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu | |
| 1 5 10 15 | |
| ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGT GCT GCC AGA | 96 |
| Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg | |
| 20 25 30 | |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAA GAC GGC GTG AAC TAT GCA | 144 |
| Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala | |
| 35 40 45 | |
| ACA GGG AAT TTG CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA | 192 |
| Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu | |
| 50 55 60 | |
| CTG TCC TGT CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG | 240 |
| Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val | |
| 65 70 75 80 | |

| | |
|---|-----|
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90 95 | 288 |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105 110 | 336 |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr 115 120 125 | 384 |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACT ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His 130 135 140 | 432 |
| GTC GAT TTG CTC GTT GGG GCG GCT TTC TGT TCC GCT ATG TAC GTG Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val 145 150 155 160 | 480 |
| GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile 165 170 175 | 528 |
| TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr 180 185 190 | 576 |
| CCC GGC CAC ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn 195 200 205 | 624 |
| TGG TAATAG Trp 210 | 633 |

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

| |
|--|
| Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu 1 5 10 15 |
|--|

| |
|---|
| Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg 20 25 30 |
|---|

| |
|---|
| Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala 35 40 45 |
|---|

| |
|---|
| Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu 50 55 60 |
|---|

Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
195 200 205

Trp

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..480

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys
1 5 10 15 48

CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG 96

| | | | |
|--|-----|-----|-----|
| Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val | | | |
| 20 | 25 | 30 | |
| TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA | | | 144 |
| Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala | | | |
| 35 | 40 | 45 | |
| GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG | | | 192 |
| Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu | | | |
| 50 | 55 | 60 | |
| GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC | | | 240 |
| Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala | | | |
| 65 | 70 | 75 | 80 |
| AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG | | | 288 |
| Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu | | | |
| 85 | 90 | 95 | |
| CTC GTT GGG GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC | | | 336 |
| Leu Val Gly Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu | | | |
| 100 | 105 | 110 | |
| TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC | | | 384 |
| Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg | | | |
| 115 | 120 | 125 | |
| CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT | | | 432 |
| Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His | | | |
| 130 | 135 | 140 | |
| GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TCC TAATAG | | | 483 |
| Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser | | | |
| 145 | 150 | 155 | 160 |

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

| | | | |
|---|----|----|----|
| Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys | | | |
| 1 | 5 | 10 | 15 |
| Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val | | | |
| 20 | 25 | 30 | |
| Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala | | | |
| 35 | 40 | 45 | |
| Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu | | | |
| 50 | 55 | 60 | |
| Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala | | | |
| 65 | 70 | 75 | 80 |

Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu
85 90 95

Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu
100 105 110

Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
115 120 125

Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His
130 135 140

Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG TCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT 48
Met Ser Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys
1 5 10 15

CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG 96
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val
20 25 30

TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA 144
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala
35 40 45

GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG 192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu
50 55 60

GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC 240
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala
65 70 75 80

| | | |
|---|-----|-----|
| AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG | | 288 |
| Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu | | |
| 85 | 90 | 95 |
| CTC GTT GGG GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC | | 336 |
| Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu | | |
| 100 | 105 | 110 |
| TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TCA CCT CGC | | 384 |
| Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg | | |
| 115 | 120 | 125 |
| CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT | | 432 |
| Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His | | |
| 130 | 135 | 140 |
| GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG AAC TGG TAATAG | | 480 |
| Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp | | |
| 145 | 150 | 155 |

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

| | | | |
|---|-----|-----|----|
| Met Ser Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys | | | |
| 1 | 5 | 10 | 15 |
| Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val | | | |
| 20 | 25 | 30 | |
| Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala | | | |
| 35 | 40 | 45 | |
| Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu | | | |
| 50 | 55 | 60 | |
| Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala | | | |
| 65 | 70 | 75 | 80 |
| Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His Val Asp Leu | | | |
| 85 | 90 | 95 | |
| Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu | | | |
| 100 | 105 | 110 | |
| Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg | | | |
| 115 | 120 | 125 | |
| Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His | | | |
| 130 | 135 | 140 | |
| Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp | | | |
| 145 | 150 | 155 | |

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

| | |
|---|-----|
| GATG CTG GGT AAG GCC ATC GAT ACC CTT ACG TGC GGC TTC GCC GAC CTC Met Leu Gly Lys Ala Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu | 48 |
| 1 5 10 15 | |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg | 96 |
| 20 25 30 | |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAA GAC GGC GTG AAC TAT GCA Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala | 144 |
| 35 40 45 | |
| ACA GGG AAT TTG CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu | 192 |
| 50 55 60 | |
| CTG TCC TGT CTA ACC ATT CCA GCT TCC GCT TAC GAG GTG CGC AAC GTG Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val | 240 |
| 65 70 75 80 | |
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val | 288 |
| 85 90 95 | |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys | 336 |
| 100 105 110 | |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr | 384 |
| 115 120 125 | |
| CTC GCG GCT AGG AAC GCC AGC ATC CCC ACT ACA ACA ATA CGA CGC CAC | 432 |

| | | | |
|---|-----|-----|-----|
| Leu Ala Ala Arg Asn Ala Ser Ile Pro Thr Thr Thr Ile Arg Arg His | | | |
| 130 | 135 | 140 | |
| GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG | | | 480 |
| Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val | | | |
| 145 | 150 | 155 | 160 |
| GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC | | | 528 |
| Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile | | | |
| 165 | 170 | 175 | |
| TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT | | | 576 |
| Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr | | | |
| 180 | 185 | 190 | |
| CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC | | | 624 |
| Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn | | | |
| 195 | 200 | 205 | |
| TGG TAC TAATAG | | | 640 |
| Trp Tyr | | | |
| 210 | | | |

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Leu Gly Lys Ala Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60

Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125

Leu Ala Ala Arg Asn Ala Ser Ile Pro Thr Thr Ile Arg Arg His

130

135

140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn
195 200 205

Trp Tyr
210

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATGCCCGGTT GCTCTTCCTC TATCTT

26

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGTTGGGTA AGGTCACTCGA TACCCCT

26

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTATTAGGAC CAGTCATCA TCATATCCCA

30

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTATTACCAAG TTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATACGACGCC ACGTCGATTC CCAGCTGTTC ACCATC

36

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GATGGTGAAC AGCTGGAAAT CGACGTGGCG TCGTAT

36

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
1 5 10 15

48

GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30

96

GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
35 40 45

144

ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60

192

CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
65 70 75 80

240

| | |
|---|-----|
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val 85 90 95 | 288 |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105 110 | 336 |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr 115 120 125 | 384 |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His 130 135 140 | 432 |
| GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val 145 150 155 160 | 480 |
| CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg 165 170 175 | 528 |
| ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val 180 185 190 | 576 |
| GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala 195 200 205 | 624 |
| GGG GCC CAT TGG GGA GTC CTG GCG GGT CTC GCC TAC TAT TCC ATG GTG Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val 210 215 220 | 672 |
| GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC TTT GCT CCC TAATAG Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro 225 230 235 240 | 723 |

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 239 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
   1           5           10          15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
   20          25          30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
   35          40          45

```

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
165 170 175

Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
180 185 190

Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala
195 200 205

Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val
210 215 220

Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro
225 230 235

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 561 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..558

- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

| | |
|--|-----|
| ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu | 48 |
| 1 5 10 15 | |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg | 96 |
| 20 25 30 | |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala | 144 |
| 35 40 45 | |
| ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu | 192 |
| 50 55 60 | |
| CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val | 240 |
| 65 70 75 80 | |
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val | 288 |
| 85 90 95 | |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys | 336 |
| 100 105 110 | |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr | 384 |
| 115 120 125 | |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His | 432 |
| 130 135 140 | |
| GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val | 480 |
| 145 150 155 160 | |
| CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg | 528 |
| 165 170 175 | |
| ATG GCT TGG GAT ATG ATG AAC TGG TAATAG Met Ala Trp Asp Met Met Asn Trp | 561 |
| 180 185 | |

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu

1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
165 170 175

Met Ala Trp Asp Met Met Asn Trp
180 185

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 606 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..603

(ix) FEATURE:
(A) NAME/KEY: mat peptide
(B) LOCATION: 1..600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

| | |
|--|-----|
| ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu | 48 |
| 1 5 10 15 | |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg | 96 |
| 20 25 30 | |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala | 144 |
| 35 40 45 | |
| ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu | 192 |
| 50 55 60 | |
| CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val | 240 |
| 65 70 75 80 | |
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val | 288 |
| 85 90 95 | |
| Q PAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CGC CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys | 336 |
| 100 105 110 | |
| Q GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr | 384 |
| 115 120 125 | |
| Q CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His | 432 |
| 130 135 140 | |
| Q GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val | 480 |
| 145 150 155 160 | |
| Q CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg | 528 |
| 165 170 175 | |
| ATG GCT TGG GAT ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val | 576 |
| 180 185 190 | |
| GTA TCG CAG CTG CTC CGG ATC CTC TAATAAG Val Ser Gln Leu Leu Arg Ile Leu | 606 |
| 195 200 | |

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 200 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His
130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val
145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg
165 170 175

Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val
180 185 190

Val Ser Gln Leu Leu Arg Ile Leu
195 200

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

| | |
|--|-----|
| ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu | 48 |
| 1 5 10 15 | |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg | 96 |
| 20 25 30 | |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala | 144 |
| 35 40 45 | |
| ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu | 192 |
| 50 55 60 | |
| CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val | 240 |
| 65 70 75 80 | |
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val | 288 |
| 85 90 95 | |
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys | 336 |
| 100 105 110 | |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr | 384 |
| 115 120 125 | |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His | 432 |
| 130 135 140 | |
| GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val | 480 |
| 145 150 155 160 | |
| CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg | 528 |
| 165 170 175 | |
| ATG GCT TGG GAT ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG Met Ala Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val | 576 |
| 180 185 190 | |
| GTA TCG CAG CTG CTC CGG ATC GTG ATC GAG GGC AGA CAC CAT CAC CAC Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His His | 624 |
| 195 200 205 | |
| CAT CAC TAATAG His His | 636 |

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu |
| 1 | | | | 5 | | | | 10 | | | | | | | 15 |
| | | | | | | | | | | | | | | | |
| Val | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | Pro | Leu | Gly | Gly | Ala | Ala | Arg |
| | | | | | 20 | | | 25 | | | | | | | 30 |
| | | | | | | | | | | | | | | | |
| Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala |
| | | | | | 35 | | | 40 | | | | | | | 45 |
| | | | | | | | | | | | | | | | |
| Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Leu | Leu | Ala | Leu |
| | | | | | 50 | | | 55 | | | | | | | 60 |
| | | | | | | | | | | | | | | | |
| Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Glu | Val | Arg | Asn | Val |
| | | | | | 65 | | | 70 | | | 75 | | | | 80 |
| | | | | | | | | | | | | | | | |
| Ser | Gly | Met | Tyr | His | Val | Thr | Asn | Asp | Cys | Ser | Asn | Ser | Ser | Ile | Val |
| | | | | | 85 | | | 90 | | | | | | | 95 |
| | | | | | | | | | | | | | | | |
| Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr | Pro | Gly | Cys | Val | Pro | Cys |
| | | | | | 100 | | | 105 | | | | | | | 110 |
| | | | | | | | | | | | | | | | |
| Val | Arg | Glu | Asn | Asn | Ser | Ser | Arg | Cys | Trp | Val | Ala | Leu | Thr | Pro | Thr |
| | | | | | 115 | | | 120 | | | | | | | 125 |
| | | | | | | | | | | | | | | | |
| Leu | Ala | Ala | Arg | Asn | Ala | Ser | Val | Pro | Thr | Thr | Ile | Arg | Arg | His | |
| | | | | | 130 | | | 135 | | | 140 | | | | |
| | | | | | | | | | | | | | | | |
| Val | Asp | Ser | Gln | Leu | Phe | Thr | Ile | Ser | Pro | Arg | Arg | His | Glu | Thr | Val |
| | | | | | 145 | | | 150 | | | 155 | | | | 160 |
| | | | | | | | | | | | | | | | |
| Gln | Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Pro | Gly | His | Ile | Thr | Gly | His | Arg |
| | | | | | 165 | | | 170 | | | | | | | 175 |
| | | | | | | | | | | | | | | | |
| Met | Ala | Trp | Asp | Met | Met | Asn | Trp | Ser | Pro | Thr | Thr | Ala | Leu | Val | |
| | | | | | 180 | | | 185 | | | | | | | 190 |
| | | | | | | | | | | | | | | | |
| Val | Ser | Gln | Leu | Leu | Arg | Ile | Val | Ile | Glu | Gly | Arg | His | His | His | His |
| | | | | | 195 | | | 200 | | | | | | | 205 |
| | | | | | | | | | | | | | | | |
| His | His | | | | | | | | | | | | | | |
| | 210 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..627

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

| | |
|--|-----|
| ATG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGA TTC GCC GAT CTC ATG Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met | 48 |
| 1 5 10 15 | |
| GGG TAC ATC CCG CTC GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala | 96 |
| 20 25 30 | |
| CTT GCG CAT GGC GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr | 144 |
| 35 40 45 | |
| GGG AAT TTG CCC GGT TGC TCC TTT TCT ATT TTC CTT CTC GCT CTG TTC Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe | 192 |
| 50 55 60 | |
| TCT TGC TTA ATT CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser | 240 |
| 65 70 75 80 | |
| GGC CTC TAT GTC CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr | 288 |
| 85 90 95 | |
| GAG GCC GAT GAC GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val | 336 |
| 100 105 110 | |
| CAG GAC GGC AAT ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val | 384 |
| 115 120 125 | |
| GCA GTC AAG TAC GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val | 432 |
| 130 135 140 | |
| GAC CTA TTA GTG GGC GCG GCC ACG ATG TGC TCT GCG CTC TAC GTG GGT Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly | 480 |
| 145 150 155 160 | |

| | |
|---|-----|
| GAC ATG TGT GGG GCT GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg 165 170 175 | 528 |
| CCT CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro 180 185 190 | 576 |
| GGC CAT CTT TCA GGA CAT CGA ATG GCT TGG GAT ATG ATG ATG AAC TGG Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Asn Trp 195 200 205 | 624 |
| TAATAG | 634 |

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
1 5 10 15

Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala
20 25 30

Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr
35 40 45

Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Ala Leu Phe
50 55 60

Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser
65 70 75 80

Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr
85 90 95

Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val
100 105 110

Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val
115 120 125

Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val
130 135 140

Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly
145 150 155 160

Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg
165 170 175

Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro
180 185 190

Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
195 200 205

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..627

- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC GCC GAT CTC ATG 48
Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
1 5 10 15

GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT GGG GGC GTC GCA AGG GCT 96
Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala
20 25 30

CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA 144
Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr
35 40 45

GGG AAT TTA CCC GGT TGC TCT TTC TCT ATC TTT ATT CTT GCT CTT CTC 192
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
50 55 60

TCG TGT CTG ACC GTT CCG GCC TCT GCA GTT CCC TAC CGA AAT GCC TCT 240
Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser
65 70 75 80

GGG ATT TAT CAT GTT ACC AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT 288
Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr
85 90 95

GAG GCA GAT AAC CTG ATC CTA CAC GCA CCT GGT TGC GTG CCT TGT GTC 336

| | | | |
|---|-----|-----|-----|
| Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val | | | |
| 100 | 105 | 110 | |
| ATG ACA GGT AAT GTG AGT AGA TGC TGG GTC CAA ATT ACC CCT ACA CTG | | | 384 |
| Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu | | | |
| 115 | 120 | 125 | |
| TCA GCC CCG AGC CTC GGA GCA GTC ACG GCT CCT CTT CGG AGA GCC GTT | | | 432 |
| Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val | | | |
| 130 | 135 | 140 | |
| GAC TAC CTA GCG GGA GGG GCT GCC CTC TGC TCC GCG TTA TAC GTA GGA | | | 480 |
| Asp Tyr Leu Ala Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly | | | |
| 145 | 150 | 155 | 160 |
| GAC GCG TGT GGG GCA CTA TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG | | | 528 |
| Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg | | | |
| 165 | 170 | 175 | |
| CCT CGC CAG CAC GCT ACG GTG CAG AAC TGC AAC TGT TCC ATT TAC AGT | | | 576 |
| Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser | | | |
| 180 | 185 | 190 | |
| GGC CAT GTT ACC GGC CAC CGG ATG GCA TGG GAT ATG ATG ATG AAC TGG | | | 624 |
| Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp | | | |
| 195 | 200 | 205 | |
| TAATAG | | | 630 |

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Lys | Val | Ile | Asp | Thr | Leu | Thr | Cys | Gly | Phe | Ala | Asp | Leu | Met |
| 1 | | | 5 | | | | 10 | | | | | | 15 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Tyr | Ile | Pro | Leu | Val | Gly | Gly | Pro | Ile | Gly | Gly | Val | Ala | Arg | Ala |
| | | | | | | 20 | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | His | Gly | Val | Arg | Val | Leu | Glu | Asp | Gly | Val | Asn | Tyr | Ala | Thr |
| | | | | | | | 35 | 40 | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | Ser | Ile | Phe | Ile | Leu | Ala | Leu | Leu |
| | | | | | | | 50 | 55 | | 60 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Val | Pro | Tyr | Arg | Asn | Ala | Ser |
| | | | | | | | 65 | 70 | | 75 | | 80 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ile | Tyr | His | Val | Thr | Asn | Asp | Cys | Pro | Asn | Ser | Ser | Ile | Val | Tyr |
| | | | | | | | 85 | 90 | | | | 95 | | | |

Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val
100 105 110

Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu
115 120 125

Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val
130 135 140

Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly
145 150 155 160

Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg
165 170 175

Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser
180 185 190

Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
195 200 205

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TGGGATATGA TGATGAAGTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CTATTATGGT GGTAAGCCAC AGAGCAGGAG

30

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1473

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1..1470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

| | |
|---|-----|
| TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser 1 5 10 15 | 48 |
| CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC Gln Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala 20 25 30 | 96 |
| CAT TGG GGA GTC CTG GCG CTC GCC TAC TAT TCC ATG GTG GGG AAC His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn 35 40 45 | 144 |
| TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly 50 55 60 | 192 |
| CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu 65 70 75 80 | 240 |
| G TG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn 85 90 95 | 288 |
| ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp 100 105 110 | 336 |
| TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe 115 120 125 | 384 |
| AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC | 432 |

| | | |
|---|-----|------|
| Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp | | |
| 130 | 135 | 140 |
| AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC | | 480 |
| Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser | | |
| 145 | 150 | 155 |
| 160 | | |
| TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT | | 528 |
| Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly | | |
| 165 | 170 | 175 |
| ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG | | 576 |
| Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro | | |
| 180 | 185 | 190 |
| AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT | | 624 |
| Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr | | |
| 195 | 200 | 205 |
| AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG | | 672 |
| Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg | | |
| 210 | 215 | 220 |
| CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG | | 720 |
| Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly | | |
| 225 | 230 | 235 |
| 240 | | |
| TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC | | 768 |
| Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly | | |
| 245 | 250 | 255 |
| AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG | | 816 |
| Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu | | |
| 260 | 265 | 270 |
| GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT | | 864 |
| Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys | | |
| 275 | 280 | 285 |
| ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC | | 912 |
| Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn | | |
| 290 | 295 | 300 |
| TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG | | 960 |
| Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg | | |
| 305 | 310 | 315 |
| 320 | | |
| TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG | | 1008 |
| Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu | | |
| 325 | 330 | 335 |
| GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG | | 1056 |
| Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu | | |
| 340 | 345 | 350 |
| TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC | | 1104 |
| Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr | | |
| 355 | 360 | 365 |
| GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC | | 1152 |
| Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr | | |
| 370 | 375 | 380 |

| | |
|---|------|
| GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val 385 390 395 400 | 1200 |
| CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA Leu Leu Leu Phe Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu 405 410 415 | 1248 |
| TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu 420 425 430 | 1296 |
| GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC Val Val Leu Asn Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser 435 440 445 | 1344 |
| TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val 450 455 460 | 1392 |
| CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu 465 470 475 480 | 1440 |
| CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala 485 490 | 1476 |

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

| |
|--|
| Trp Asp Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser 1 5 10 15 |
| Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala 20 25 30 |
| His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn 35 40 45 |
| Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly 50 55 60 |
| His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu 65 70 75 80 |
| Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn 85 90 95 |
| Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp 100 105 110 |

435

440

445

Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val
 450 455 460

Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu
 465 470 475 480

Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala
 485 490

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1018

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..1015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

| | |
|---|----|
| G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA | 46 |
| Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly | |
| 1 5 10 15 | |

| | |
|---|----|
| GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG | 94 |
| Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys | |
| 20 25 30 | |

| | |
|---|-----|
| GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC | 142 |
| Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg | |
| 35 40 45 | |

| | |
|---|-----|
| GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC | 190 |
| Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu | |
| 50 55 60 | |

| | |
|---|-----|
| TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC | 238 |
| Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly | |
| 65 70 75 | |

| | |
|---|-----|
| AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA | 286 |
| Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln | |
| 80 85 90 95 | |

| | |
|--|------|
| ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser | 334 |
| 100 105 110 | |
| GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala | 382 |
| 115 120 125 | |
| CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln | 430 |
| 130 135 140 | |
| AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro | 478 |
| 145 150 155 | |
| GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val | 526 |
| 160 165 170 175 | |
| GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly | 574 |
| 180 185 190 | |
| GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg | 622 |
| 195 200 205 | |
| GCG AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys | 670 |
| 210 215 220 | |
| ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC Thr Cys Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr | 718 |
| 225 230 235 | |
| TTG ACC TGC CCC ACT GAC TGT TTT CCG AAG CAC CCC GAG GCC ACC TAC Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr | 766 |
| 240 245 250 255 | |
| GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His | 814 |
| 260 265 270 | |
| TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile | 862 |
| 275 280 285 | |
| TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala | 910 |
| 290 295 300 | |
| GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp | 958 |
| 305 310 315 | |
| AGA TCA GAG CTT AGC CCG CTG CTG TCT ACA ACA GAG TGG CAG AGT Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp Gln Ser | 1006 |
| 320 325 330 335 | |
| GGC AGA GCT TAATTA | 1021 |

Gly Arg Ala

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val
1 5 10 15

Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
20 25 30

Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val
35 40 45

Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe
50 55 60

Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser
65 70 75 80

Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr
85 90 95

Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly
100 105 110

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln
115 120 125

Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg
130 135 140

Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala
145 150 155 160

Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val
165 170 175

Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala
180 185 190

Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly
195 200 205

Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr
210 215 220

Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu
225 230 235 240

Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala
245 250 255

Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr
260 265 270

Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe
275 280 285

Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala
290 295 300

Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg
305 310 315 320

Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly
325 330 335

Arg Ala

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1034 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..1032

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 2..1029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA 46
Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly
1 5 10 15

GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG 94
Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys
20 25 30

GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC 142
Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg
35 40 45

GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC 190
Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu
50 55 60

Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe
115 120 125

Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp
130 135 140

Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser
145 150 155 160

Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly
165 170 175

Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro
180 185 190

Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr
195 200 205

Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg
210 215 220

Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly
225 230 235 240

Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly
245 250 255

Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu
260 265 270

Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys
275 280 285

Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn
290 295 300

Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg
305 310 315 320

Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu
325 330 335

Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu
340 345 350

Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr
355 360 365

Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr
370 375 380

Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val
385 390 395 400

Leu Leu Leu Phe Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu
405 410 415

Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu
420 425 430

Val Val Leu Asn Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser

| | |
|---|-----|
| TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly 65 70 75 | 238 |
| AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln 80 85 90 95 | 286 |
| ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser 100 105 110 | 334 |
| GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala 115 120 125 | 382 |
| CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln 130 135 140 | 430 |
| AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro 145 150 155 | 478 |
| GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val 160 165 170 175 | 526 |
| G GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly 180 185 190 | 574 |
| GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg 195 200 205 | 622 |
| GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys 210 215 220 | 670 |
| ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr 225 230 235 | 718 |
| TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr 240 245 250 255 | 766 |
| GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His 260 265 270 | 814 |
| TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile 275 280 285 | 862 |
| TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala 290 295 300 | 910 |
| GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp | 958 |

| | | | |
|---|-----|-----|------|
| 305 | 310 | 315 | |
| AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG | | | 1006 |
| Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Gly Asp Arg Gly | | | |
| 320 | 325 | 330 | 335 |
| CAG ACA CCA TCA CCA CCA TCA CTA AT AG | | | 1034 |
| Gln Thr Pro Ser Pro Pro Ser Leu | | | |
| 340 | | | |

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

| | | | |
|---|-----|-----|-----|
| Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val | | | |
| 1 | 5 | 10 | 15 |
| Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val | | | |
| 20 | 25 | 30 | |
| Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val | | | |
| 35 | 40 | 45 | |
| Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe | | | |
| 50 | 55 | 60 | |
| Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser | | | |
| 65 | 70 | 75 | 80 |
| Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr | | | |
| 85 | 90 | 95 | |
| Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly | | | |
| 100 | 105 | 110 | |
| Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln | | | |
| 115 | 120 | 125 | |
| Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg | | | |
| 130 | 135 | 140 | |
| Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala | | | |
| 145 | 150 | 155 | 160 |
| Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val | | | |
| 165 | 170 | 175 | |
| Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala | | | |
| 180 | 185 | 190 | |
| Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly | | | |
| 195 | 200 | 205 | |

Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr
 210 215 220

Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu
 225 230 235 240

Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala
 245 250 255

Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr
 260 265 270

Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe
 275 280 285

Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala
 290 295 300

Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg
 305 310 315 320

Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Gly Asp Arg Gly Gln
 325 330 335

Thr Pro Ser Pro Pro Ser Leu
 340

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 945 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..942

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

| | |
|---|----|
| ATG GTG GGG AAC TGG GCT AAG GTT TTG GTG ATG CTA CTC TTT GCC | 48 |
| Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala | |
| 1 5 10 15 | |
| GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT | 96 |
| Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp | |
| 20 25 30 | |

| | |
|--|-----|
| ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile | 144 |
| 35 40 45 | |
| CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu | 192 |
| 50 55 60 | |
| AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr | 240 |
| 65 70 75 80 | |
| AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys | 288 |
| 85 90 95 | |
| CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr | 336 |
| 100 105 110 | |
| GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro | 384 |
| 115 120 125 | |
| CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr | 432 |
| 130 135 140 | |
| TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly | 480 |
| 145 150 155 160 | |
| GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu | 528 |
| 165 170 175 | |
| AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met | 576 |
| 180 185 190 | |
| AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile | 624 |
| 195 200 205 | |
| GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg | 672 |
| 210 215 220 | |
| AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu | 720 |
| 225 230 235 240 | |
| ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro | 768 |
| 245 250 255 | |
| TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly | 816 |
| 260 265 270 | |
| GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT | 864 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | His | Arg | Phe | Glu | Ala | Ala | Cys | Asn | Trp | Thr | Arg | Gly | Glu | Arg |
| 275 | | | | | 280 | | | | | | | 285 | | | |
| TGT | GAC | TTG | GAG | GAC | AGG | GAT | AGA | TCA | GAG | CTT | AGC | CCG | CTG | CTG | CTG |
| Cys | Asp | Leu | Glu | Asp | Arg | Asp | Arg | Ser | Glu | Leu | Ser | Pro | Leu | Leu | Leu |
| 290 | | | | | 295 | | | | | | | 300 | | | |
| TCT | ACA | ACA | GAG | TGG | CAG | AGC | TTA | ATT | AAT | TAG | | | | | 912 |
| Ser | Thr | Thr | Glu | Trp | Gln | Ser | Leu | Ile | Asn | | | | | | |
| 305 | | | | | 310 | | | | | | | | | | 945 |

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Gly | Asn | Trp | Ala | Lys | Val | Leu | Val | Met | Leu | Leu | Phe | Ala | |
| 1 | | | | | 5 | | | | 10 | | | | | 15 | |
| Gly | Val | Asp | Gly | His | Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Ala | Ser | Asp |
| | | | | | 20 | | | 25 | | | | | | 30 | |
| Thr | Arg | Gly | Leu | Val | Ser | Leu | Phe | Ser | Pro | Gly | Ser | Ala | Gln | Lys | Ile |
| | | | | | 35 | | | 40 | | | | | | 45 | |
| Gln | Leu | Val | Asn | Thr | Asn | Gly | Ser | Trp | His | Ile | Asn | Arg | Thr | Ala | Leu |
| | | | | | 50 | | | 55 | | | | | | 60 | |
| Asn | Cys | Asn | Asp | Ser | Leu | Gln | Thr | Gly | Phe | Phe | Ala | Ala | Leu | Phe | Tyr |
| | | | | | 65 | | | 70 | | | | | | 80 | |
| Lys | His | Lys | Phe | Asn | Ser | Ser | Gly | Cys | Pro | Glu | Arg | Leu | Ala | Ser | Cys |
| | | | | | 85 | | | 90 | | | | | | 95 | |
| Arg | Ser | Ile | Asp | Lys | Phe | Ala | Gln | Gly | Trp | Gly | Pro | Leu | Thr | Tyr | Thr |
| | | | | | 100 | | | 105 | | | | | | 110 | |
| Glu | Pro | Asn | Ser | Ser | Asp | Gln | Arg | Pro | Tyr | Cys | Trp | His | Tyr | Ala | Pro |
| | | | | | 115 | | | 120 | | | | | | 125 | |
| Arg | Pro | Cys | Gly | Ile | Val | Pro | Ala | Ser | Gln | Val | Cys | Gly | Pro | Val | Tyr |
| | | | | | 130 | | | 135 | | | | | | 140 | |
| Cys | Phe | Thr | Pro | Ser | Pro | Val | Val | Gly | Thr | Thr | Asp | Arg | Phe | Gly | |
| | | | | | 145 | | | 150 | | | | | | 160 | |
| Val | Pro | Thr | Tyr | Asn | Trp | Gly | Ala | Asn | Asp | Ser | Asp | Val | Leu | Ile | Leu |
| | | | | | 165 | | | 170 | | | | | | 175 | |
| Asn | Asn | Thr | Arg | Pro | Pro | Arg | Gly | Asn | Trp | Phe | Gly | Cys | Thr | Trp | Met |
| | | | | | 180 | | | 185 | | | | | | 190 | |
| Asn | Gly | Thr | Gly | Phe | Thr | Lys | Thr | Cys | Gly | Gly | Pro | Pro | Cys | Asn | Ile |
| | | | | | 195 | | | 200 | | | | | | 205 | |

Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg
210 215 220

Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu
225 230 235 240

Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro
245 250 255

Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly
260 265 270

Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg
275 280 285

Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu
290 295 300

Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn
305 310

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..958

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC 48
Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala
1 5 10 15

GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT 96
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ser Asp
20 25 30

ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC 144
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile
35 40 45

CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG 192

| | | | |
|---|-----|-----|-----|
| Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu | | | |
| 50 | 55 | 60 | |
| AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC | | | 240 |
| Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr | | | |
| 65 | 70 | 75 | 80 |
| AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT | | | 288 |
| Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys | | | |
| 85 | 90 | 95 | |
| CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT | | | 336 |
| Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr | | | |
| 100 | 105 | 110 | |
| GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT | | | 384 |
| Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro | | | |
| 115 | 120 | 125 | |
| CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT | | | 432 |
| Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr | | | |
| 130 | 135 | 140 | |
| TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT | | | 480 |
| Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly | | | |
| 145 | 150 | 155 | 160 |
| GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC | | | 528 |
| Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu | | | |
| 165 | 170 | 175 | |
| AAC AAC ACG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG | | | 576 |
| Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met | | | |
| 180 | 185 | 190 | |
| AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC | | | 624 |
| Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile | | | |
| 195 | 200 | 205 | |
| GGG GGG GCC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG | | | 672 |
| Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg | | | |
| 210 | 215 | 220 | |
| AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG | | | 720 |
| Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu | | | |
| 225 | 230 | 235 | 240 |
| ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC | | | 768 |
| Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro | | | |
| 245 | 250 | 255 | |
| TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC | | | 816 |
| Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly | | | |
| 260 | 265 | 270 | |
| GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT | | | 864 |
| Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg | | | |
| 275 | 280 | 285 | |
| TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG | | | 912 |
| Cys Asp Leu Glu Asp Arg Asp Ser Glu Leu Ser Pro Leu Leu Leu | | | |

| | | | |
|---|-----|-----|-----|
| 290 | 295 | 300 | |
| TCT ACA ACA GGT GAT CGA GGG CAG ACA CCA TCA CCA CCA TCA CTA A | | | 958 |
| Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu | | | |
| 305 | 310 | 315 | |
| TAG | | | 961 |

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

| | | | |
|---|-----|-----|-----|
| Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala | | | |
| 1 | 5 | 10 | 15 |
| Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp | | | |
| 20 | 25 | 30 | |
| Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile | | | |
| 35 | 40 | 45 | |
| Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu | | | |
| 50 | 55 | 60 | |
| Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr | | | |
| 65 | 70 | 75 | 80 |
| Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys | | | |
| 85 | 90 | 95 | |
| Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr | | | |
| 100 | 105 | 110 | |
| Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro | | | |
| 115 | 120 | 125 | |
| Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr | | | |
| 130 | 135 | 140 | |
| Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly | | | |
| 145 | 150 | 155 | 160 |
| Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu | | | |
| 165 | 170 | 175 | |
| Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met | | | |
| 180 | 185 | 190 | |
| Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile | | | |
| 195 | 200 | 205 | |
| Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg | | | |
| 210 | 215 | 220 | |
| Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu | | | |

| | | | |
|---|-----|-----|-----|
| 225 | 230 | 235 | 240 |
| Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro | | | |
| 245 | | 250 | 255 |
| Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly | | | |
| 260 | | 265 | 270 |
| Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg | | | |
| 275 | 280 | | 285 |
| Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu | | | |
| 290 | 295 | | 300 |
| Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu | | | |
| 305 | 310 | | 315 |

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1392

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

| | |
|---|-----|
| ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT | 48 |
| Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr | |
| 1 5 10 15 | |
| TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT | 96 |
| Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Met Leu Leu Phe | |
| 20 25 30 | |
| GCC GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC | 144 |
| Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser | |
| 35 40 45 | |
| GAT ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA | 192 |
| Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys | |
| 50 55 60 | |
| ATC CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC | 240 |
| Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala | |
| 65 70 75 80 | |

| | |
|---|------|
| CTG AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe 85 90 95 | 288 |
| TAC AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser 100 105 110 | 336 |
| TGT CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr 115 120 125 | 384 |
| ACT GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala 130 135 140 | 432 |
| CCT CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val 145 150 155 160 | 480 |
| TAT TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe 165 170 175 | 528 |
| GGT GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile 180 185 190 | 576 |
| CTC AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp 195 200 205 | 624 |
| ATG AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn 210 215 220 | 672 |
| ATC GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe 225 230 235 240 | 720 |
| CGG AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp 245 250 255 | 768 |
| CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr 260 265 270 | 816 |
| CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly 275 280 285 | 864 |
| GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu 290 295 300 | 912 |
| CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu 305 310 315 320 | 960 |
| CTG TCT ACA ACA GAG TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG | 1008 |

| | | | |
|--|-----|-----|------|
| Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu | | | |
| 325 | 330 | 335 | |
| CCG GCC CTA TCC ACC GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC | | | 1056 |
| Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp | | | |
| 340 | 345 | 350 | |
| GTG CAA TAC CTG TAC GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC | | | 1104 |
| Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile | | | |
| 355 | 360 | 365 | |
| AAA TGG GAG TAT GTC CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC | | | 1152 |
| Lys Trp Glu Tyr Val Leu Leu Phe Leu Leu Ala Asp Ala Arg | | | |
| 370 | 375 | 380 | |
| ATC TGC GCC TGC TTA TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC | | | 1200 |
| Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ala Gln Ala Glu Ala | | | |
| 385 | 390 | 395 | 400 |
| GCC TTA GAG AAC CTG GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG | | | 1248 |
| Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala | | | |
| 405 | 410 | 415 | |
| CAT GGC ACT CTT TCC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC | | | 1296 |
| His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile | | | |
| 420 | 425 | 430 | |
| AAG GGC AGG CTG GTC CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG | | | 1344 |
| Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp | | | |
| 435 | 440 | 445 | |
| CCG CTG CTC CTG CTT CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA | | | 1395 |
| Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala | | | |
| 450 | 455 | 460 | |

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

| | | | |
|---|----|----|----|
| Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr | | | |
| 1 | 5 | 10 | 15 |
| Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe | | | |
| 20 | 25 | 30 | |
| Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser | | | |
| 35 | 40 | 45 | |
| Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys | | | |
| 50 | 55 | 60 | |
| Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala | | | |
| 65 | 70 | 75 | 80 |

Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe
85 90 95

Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser
100 105 110

Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr
115 120 125

Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala
130 135 140

Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val
145 150 155 160

Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe
165 170 175

Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile
180 185 190

Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp
195 200 205

Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn
210 215 220

Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe
225 230 235 240

Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp
245 250 255

Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr
260 265 270

Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly
275 280 285

Lys Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu
290 295 300 305

Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu
310 315 320

Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu
325 330 335

Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp
340 345 350

Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile
355 360 365

Lys Trp Glu Tyr Val Leu Leu Phe Leu Leu Ala Asp Ala Arg
370 375 380

Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala
385 390 395 400

Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Val Ala Gly Ala

| | | |
|---|-----|-----|
| 405 | 410 | 415 |
| His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile | | |
| 420 | 425 | 430 |
| Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp | | |
| 435 | 440 | 445 |
| Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala | | |
| 450 | 455 | 460 |

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2079

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..2076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

| | |
|---|-----|
| AT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC | 48 |
| sn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu | |
| 1 5 10 15 | |
| GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG | 96 |
| Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg | |
| 20 25 30 | |
| GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA | 144 |
| Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala | |
| 35 40 45 | |
| ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG | 192 |
| Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu | |
| 50 55 60 | |
| CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG | 240 |
| Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val | |
| 65 70 75 80 | |
| TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG | 288 |
| Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val | |
| 85 90 95 | |

| | |
|---|------|
| TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys 100 105 110 | 336 |
| GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr 115 120 125 | 384 |
| CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His 130 135 140 | 432 |
| GTG GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG Val Asp Leu Leu Val Gly Ala Ala Phe Cys Ser Ala Met Tyr Val 145 150 155 160 | 480 |
| GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile 165 170 175 | 528 |
| TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr 180 185 190 | 576 |
| CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn 195 200 205 | 624 |
| GGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro 210 215 220 | 672 |
| CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala 225 230 235 240 | 720 |
| GCG CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val 245 250 255 | 768 |
| GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly 260 265 270 | 816 |
| GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro 275 280 285 | 864 |
| GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His 290 295 300 | 912 |
| ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe 305 310 315 320 | 960 |
| TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro 325 330 335 | 1008 |
| GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG | 1056 |

| | | | |
|---|-----|-----|------|
| Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp | | | |
| 340 | 345 | 350 | |
| GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC | | | 1104 |
| Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr | | | |
| 355 | 360 | 365 | |
| TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG | | | 1152 |
| Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln | | | |
| 370 | 375 | 380 | |
| GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG | | | 1200 |
| Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly | | | |
| 385 | 390 | 395 | 400 |
| ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC | | | 1248 |
| Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp | | | |
| 405 | 410 | 415 | |
| TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG | | | 1296 |
| Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp | | | |
| 420 | 425 | 430 | |
| TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG | | | 1344 |
| Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly | | | |
| 435 | 440 | 445 | |
| GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC | | | 1392 |
| Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys | | | |
| 450 | 455 | 460 | |
| CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC | | | 1440 |
| Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys | | | |
| 465 | 470 | 475 | 480 |
| GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT | | | 1488 |
| Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr | | | |
| 485 | 490 | 495 | |
| AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT | | | 1536 |
| Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val | | | |
| 500 | 505 | 510 | |
| AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT | | | 1584 |
| Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn | | | |
| 515 | 520 | 525 | |
| TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG | | | 1632 |
| Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu | | | |
| 530 | 535 | 540 | |
| CTT AGC CCG CTG CTG TCT ACA ACA GAG TGG CAG ATA CTG CCC TGT | | | 1680 |
| Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys | | | |
| 545 | 550 | 555 | 560 |
| TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC GGC CTG ATC CAC CTC CAT | | | 1728 |
| Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His | | | |
| 565 | 570 | 575 | |
| CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC GGT GTA GGG TCG GCG GTT | | | 1776 |
| Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val | | | |
| 580 | 585 | 590 | |

| | | | | |
|--|-----|-----|-----|------|
| GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC CTG TTG CTC TTC CTT CTC Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu | 595 | 600 | 605 | 1824 |
| CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA TGG ATG ATG CTG CTG ATA Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile | 610 | 615 | 620 | 1872 |
| GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG GTG GTC CTC AAT GCG GCG Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala | 625 | 630 | 635 | 1920 |
| GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC TTC CTT GTG TTC TTC TGT Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys | 645 | 650 | 655 | 1968 |
| GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC CCT GGT GCG GCA TAC GCC Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala | 660 | 665 | 670 | 2016 |
| TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT CTG CTG GCC TTA CCA CCA Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro | 675 | 680 | 685 | 2064 |
| CGA GCT TAT GCC TAGTAA Arg Ala Tyr Ala | 690 | | | 2082 |

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 692 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu
'1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg
20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala
35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu
50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val
65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val
85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys
100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr
115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His
130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val
145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile
165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr
180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn
195 200 205

Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
210 215 220

Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala
225 230 235 240

Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val
245 250 255

Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly
260 265 270

Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro
275 280 285

Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His
290 295 300

Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe
305 310 315 320

Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro
325 330 335

Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp
340 345 350

Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr
355 360 365

Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln
370 375 380

Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly
385 390 395 400

Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp
405 410 415

Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp
420 425 430

Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly

435

440

445

Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys
450 455 460

Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys
465 470 475 480

Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr
485 490 495

Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val
500 505 510

Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn
515 520 525

Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu
530 535 540

Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys
545 550 555 560

Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His
565 570 575

Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val
580 585 590

Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Phe Leu Leu
595 600 605

Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile
610 615 620

Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala
625 630 635 640

Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys
645 650 655

Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala
660 665 670

Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro
675 680 685

Arg Ala Tyr Ala
690

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2430

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..2427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

| | |
|--|-----|
| ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn | 48 |
| 1 5 10 15 | |
| CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly | 96 |
| 20 25 30 | |
| GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala | 144 |
| 35 40 45 | |
| ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGG AGG CGA CAA CCT Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro | 192 |
| 50 55 60 | |
| ATC CCC AAG GCT CGC CGA CCC GAG GGT AGG GCC TGG GCT CAG CCC GGG Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly | 240 |
| 65 70 75 80 | |
| TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG GGG TGG GCA GGA TGG Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp | 288 |
| 85 90 95 | |
| CTC CTG TCA CCC CGC GGC TCT CGG CCT AGT TGG GGC CCT ACA GAC CCC Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro | 336 |
| 100 105 110 | |
| CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys | 384 |
| 115 120 125 | |
| GGC TTC GCC GAC CTC GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu | 432 |
| 130 135 140 | |
| GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp | 480 |
| 145 150 155 160 | |
| GGC GTG AAC TAT GCA ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile | 528 |
| 165 170 175 | |
| TTC CTC TTG GCT TTG CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr | 576 |

| 180 | 185 | 190 | |
|---|-----|-----|------|
| GAA GTG CGC AAC GTG TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser 195 | 200 | 205 | 624 |
| AAC TCA AGC ATT GTG TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro 210 | 215 | 220 | 672 |
| GGG TGC GTG CCC TGC GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val 225 | 230 | 235 | 720 |
| GCG CTC ACC CCC ACG CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr 245 | 250 | 255 | 768 |
| ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys 260 | 265 | 270 | 816 |
| TCC GCT ATG TAC GTG GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser 275 | 280 | 285 | 864 |
| CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys 290 | 295 | 300 | 912 |
| AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp 305 | 310 | 315 | 960 |
| GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG Asp Met Met Asn Trp Ser Pro Thr Ala Leu Val Val Ser Gln 325 | 330 | 335 | 1008 |
| CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His 340 | 345 | 350 | 1056 |
| TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp 355 | 360 | 365 | 1104 |
| GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His 370 | 375 | 380 | 1152 |
| ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG Thr Arg Val Ser Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val 385 | 390 | 395 | 1200 |
| TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr 405 | 410 | 415 | 1248 |
| AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser 420 | 425 | 430 | 1296 |

| | |
|---|------|
| CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn 435 440 445 | 1344 |
| TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys 450 455 460 | 1392 |
| TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser 465 470 475 480 | 1440 |
| GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile 485 490 495 | 1488 |
| GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser 500 505 510 | 1536 |
| CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn 515 520 525 | 1584 |
| TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro 530 535 540 | 1632 |
| CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe 545 550 555 560 | 1680 |
| ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn 565 570 575 | 1728 |
| AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala 580 585 590 | 1776 |
| ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met 595 600 605 | 1824 |
| GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe 610 615 620 | 1872 |
| ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe 625 630 635 640 | 1920 |
| GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp 645 650 655 | 1968 |
| AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG TGG Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp 660 665 670 | 2016 |

| | |
|---|------|
| CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC GGC Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly 675 680 685 | 2064 |
| CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC GGT Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly 690 695 700 | 2112 |
| GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC CTG Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu 705 710 715 720 | 2160 |
| TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA TGG Leu Leu Phe Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp 725 730 735 | 2208 |
| ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG GTG Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val 740 745 750 | 2256 |
| GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC TTC Val Leu Asn Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe 755 760 765 | 2304 |
| CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC CCT Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro 770 775 780 | 2352 |
| GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT CTG Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu 785 790 795 800 | 2400 |
| CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA Leu Ala Leu Pro Pro Arg Ala Tyr Ala 805 810 | 2433 |

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 809 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

| |
|--|
| Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15 |
| Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly 20 25 30 |
| Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala 35 40 45 |
| Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60 |
| Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly 65 70 75 80 |

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125

Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
130 135 140

Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175

Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr
180 185 190

Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser
195 200 205

Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro
210 215 220

Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val
225 230 235 240

Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr
245 250 255

Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Phe Cys
260 265 270

Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser
275 280 285

Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys
290 295 300

Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp
305 310 315 320

Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln
325 330 335

Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His
340 345 350

Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp
355 360 365

Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His
370 375 380

Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val
385 390 395 400

Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr
405 410 415

Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser
420 425 430

Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn
435 440 445

Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys
450 455 460

Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser
465 470 475 480

Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile
485 490 495

Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser
500 505 510

Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn
515 520 525

Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro
530 535 540

Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe
545 550 555 560

Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn
565 570 575

Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala
580 585 590

Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met
595 600 605

Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe
610 615 620

Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe
625 630 635 640

Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp
645 650 655

Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Ser Thr Thr Glu Trp
660 665 670

Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly
675 680 685

Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly
690 695 700

Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu
705 710 715 720

Leu Leu Phe Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp

725 730 735

Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val
740 745 750

Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe
755 760 765

Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro
770 775 780

Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu
785 790 795 800

Leu Ala Leu Pro Pro Arg Ala Tyr Ala
805

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys
1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp

1

5

10

15

Ser Pro Thr Thr Ala Leu
20

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
1 5 10 15

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr
20 25 30

Pro Gly Cys Gly Lys
35

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr
1 5 10 15

Gln Leu Arg Arg His Ile Asp Leu Leu
20 25

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gly | Thr | Pro | Thr | Leu | Ala | Ala | Arg | Asp | Ala | Ser | Val | Pro | Thr | Thr |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Thr | Ile | Arg | Arg | His | Val | Asp | Leu | Leu | | | | | | | |
| | | 20 | | | | | 25 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | Ala | Tyr | Gln | Val | Arg | Asn |
| 1 | | | | | 5 | | | | 10 | | | | | 15 | |
| Ser | Thr | Gly | Leu | | | | | | | | | | | | |
| | | 20 | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Arg | Asn | Ser | Thr | Gly | Leu | Tyr | His | Val | Thr | Asn | Asp | Cys | Pro |
| 1 | | | | | 5 | | | 10 | | | | | | 15 | |
| Asn | Ser | Ser | Ile | | | | | | | | | | | | |
| | | 20 | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Asp | Cys | Pro | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | His | Asp | Ala | Ile |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Leu | His | Thr | Pro | | | | | | | | | | | | |
| | | | 20 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | Ala | Asp | Met | Ile | Met | His | Thr |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Pro | Gly | Cys | Val | | | | | | | | | | | | |
| | | | 20 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Asp | Ala | Ile | Leu | His | Thr | Pro | Gly | Val | Pro | Cys | Val | Arg | Glu | Gly |
| 1 | | | | 5 | | | | | 10 | | | | 15 | | |
| Asn | Val | Ser | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Cys Val Arg Glu Gly Asn Val Ser Arg Cys Trp Val Ala Met Thr Pro
1 5 10 15

Thr Val Ala Thr
20

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr
1 5 10 15

Gln Leu Arg Arg
20

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser
1 5 10 15

Ala Thr Leu Cys
20

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Leu Val Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu
1 5 10 15
Cys Gly Ser Val
20

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Gly Cys
1 5 10 15
Asn Cys Ser Ile
20

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His
1 5 10 15
Arg Met Ala Trp
20

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Ile Thr Gly His Arg Met Ala Trp Asp Met Met Asn Trp Ser Pro
1 5 10 15

Thr Ala Ala Leu
20

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile
1 5 10 15

Pro Gln Ala Ile
20

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His
1 5 10 15

Trp Gly Val Leu
20

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met
1 5 10 15
Val Gly Asn Met
20

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala Glu Thr Ile Val Ser
1 5 10 15
Gly Gly Gln Ala
20

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Gly Leu Val Ser Leu Phe Thr Pro Gly Ala Lys Gln Asn Ile Gln
1 5 10 15
Leu Ile Asn Thr
20

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Gln Trp His Ile Asn Ser
1 5 10 15

Thr Ala Leu Asn
20

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Trp Leu Ala Gly Leu
1 5 10 15

Ile Tyr Gln His Lys
20

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu
1 5 10 15

Arg Leu Ala Ser
20

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp
1 5 10 15

Gln Gly Trp Gly
20

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser
1 5 10 15

Gly Pro Asp Gln
20

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala Asn Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro
1 5 10 15

Pro Lys Pro Cys
20

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Trp His Tyr Pro Pro Lys Pro Cys Gly Ile Val Pro Ala Lys Ser Val
1 5 10 15

Cys Gly Pro Val
20

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ala Lys Ser Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val
1 5 10 15

Val Val Gly Thr
20

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Ser Gly Ala Pro Thr
1 5 10 15

Tyr Ser Trp Gly
20

(2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:
Gly Ala Pro Thr Tyr Ser Trp Gly Glu Asn Asp Thr Asp Val Phe Val
1 5 10 15

Leu Asn Asn Thr
20

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe Thr Lys
1 5 10 15

Val Cys Gly Ala
20

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Gly Phe Thr Lys Val Cys Gly Ala Pro Pro Val Cys Ile Gly Gly Ala
1 5 10 15

Gly Asn Asn Thr
20

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Ile Gly Gly Ala Gly Asn Asn Thr Leu His Cys Pro Thr Asp Cys Arg
1 5 10 15

Lys His Pro

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly
1 5 10 15

Ser Gly Pro Trp
20

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp
1 5 10 15

Tyr Pro Tyr Arg
20

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile

1

5

10

15

Asn Tyr Thr Ile
20

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Pro Cys Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly
1 5 10 15

Gly Val Glu His
20

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Met Tyr Val Gly Gly Val Glu His Arg Leu Glu Ala Ala Cys Asn Trp
1 5 10 15

Thr Pro Gly Glu
20

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ala Cys Asn Trp Thr Pro Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp
1 5 10 15

Arg Ser Glu Leu
20

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Thr Thr Thr
1 5 10 15

Gln Trp Gln Val
20

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr Gln Val Arg Asn Ser Thr Gly Leu
1 5

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ACGTCCGTAC GTTCGAATTA ATTAATCGA

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CCTCCGGACG TGCAGTAGCT CCCGTCTGTG GTAGTGGTGG TAGTGATTAT CAATTAATTG

60

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GTTTAACCAC TGCATGATG

19

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GTCCCCATCGA GTGCGGGCTAC

20

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CGTGACATGG TACATTCCGG ACACATTGGCG CACTTCATAAA GCGGA

45

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TGCCTCATAAC ACAATGGAGC TCTGGGACGA GTCGTTCGTG AC

42

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TACCCAGCAG CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC

42

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TGTCGTGGTG GGGACGGAGG CCTGCCTAGC TGCGAGCGTG GG

42

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CGTTATGTGG CCCGGGTAGA TTGAGCACTG GCAGTCCTGC ACCGTCTC

48

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CAGGGCCGTT CTAGGCCTCC ACTGCATCAT CATATCCCAA GC

42

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CCGGAATGTA CCATGTCACG AACGAC

26

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GCTCCATTGT GTATGAGGCA GCGG

24

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GAGCTCCCGC TGCTGGGTAG CGC

23

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CCTCCGTCCC CACCACGACA ATACG

25

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CTACCCGGGC CACATAACGG GTCACCG

27

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGAGGCCTAC AACGGCCCTG GTGG

24

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTCTATCGAT TAAATAGAAT TC

22

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

= GCCATACGCT CACAGCCGAT CCC

23